SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-2.p2n.rnpbm.

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-2.p2n.rnpbm.

start

```
                         GenCore version 5.1.9
              Copyright (c) 1993  - 2006  Biocceleration Ltd.


OM protein - nucleic search, using frame_plus_p2n model

Run on:          August  7, 2006, 14:46:45 ; Search time 1495 Seconds
                                             (without alignments)
                                             5868.476 Million cell updates/sec

Title:           US -10-679-362-2
Perfect score:   2469
Sequence:        1 MSTQRLRNEDYHDYSSTDVS..........YELIQPSNAPIFINSTCAFI 476

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:      37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model  -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10679362/runat_07082006_113052_26046/app_query.fasta_1
-DB=Published_Applications_NA_Main  -QFMT=fastap  -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10679362_@CGN_1_1_2530_@runat_07082006_113052_26046  -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       Published_Applications_NA_Main:*
                 1:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 6:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 7:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 8:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 9:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
```

```
12:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2469	100.0	1597	7	US -10-120-988-9	Sequence 9, Appli
2	2469	100.0	2055	7	US -10-225-810-5	Sequence 5, Appli
3	2469	100.0	2093	3	US-09-805-456-1	Sequence 1, Appli
4	2469	100.0	2093	8	US -10-679-362-1	Sequence 1, Appli
5	2469	100.0	5821	10	US -10-887-553A-1194	Sequence 1194, Ap
6	2460	99.6	1501	7	US -10-080-334-21	Sequence 21, Appl
7	2402.5	97.3	3114	8	US -10-332-447-40	Sequence 40, Appl
8	2398	97.1	1513	7	US -10-080-334-19	Sequence 19, Appl
9	2217	89.8	1961	7	US -10-094-749-1437	Sequence 1437, Ap
10	2146.5	86.9	1824	7	US -10-225-810-42	Sequence 42, Appl
11	2137.5	86.6	2034	7	US -10-225-810-2	Sequence 2, Appli
12	1722.5	69.8	3434	7	US -10-225-810-3	Sequence 3, Appli
13	1718.5	69.6	1464	7	US -10-392-219-1	Sequence 1, Appli
14	1718.5	69.6	2142	8	US -10-467-685-27	Sequence 27, Appl
15	1697.5	68.8	2456	7	US -10-225-810-13	Sequence 13, Appl
16	1676.5	67.9	2436	7	US -10-225-810-6	Sequence 6, Appli
17	1676.5	67.9	2436	7	US -10-225-810-55	Sequence 55, Appl
18	1476.5	59.8	1703	7	US -10-225-810-4	Sequence 4, Appli
19	1452.5	58.8	1473	6	US -10-291-737-1	Sequence 1, Appli
20	1452.5	58.8	1473	7	US -10-365-564-1	Sequence 1, Appli
21	1420	57.5	1752	7	US -10-225-810-1	Sequence 1, Appli
22	1333.5	54.0	947	9	US -10-357-930-23233	Sequence 23233, A
23	1333.5	54.0	947	9	US -10-357-930-29106	Sequence 29106, A
24	1263	51.2	953	7	US -10-080-334-23	Sequence 23, Appl
25	1255.5	50.9	1455	6	US -10-055-025-3	Sequence 3, Appli
26	1255.5	50.9	1455	7	US -10-154-419-93	Sequence 93, Appl
27	1255.5	50.9	1455	16	US -11-043-889-53	Sequence 53, Appl
28	1255.5	50.9	2397	6	US -10-055-025-1	Sequence 1, Appli
29	1255.5	50.9	2397	7	US -10-154-419-91	Sequence 91, Appl
30	1255.5	50.9	2397	16	US -11-043-889-51	Sequence 51, Appl
31	1255.5	50.9	2423	6	US -10-098-841-260	Sequence 260, App
32	1255.5	50.9	2905	8	US -10-755-889-21	Sequence 21, Appl
33	1255.5	50.9	3038	7	US -10-168-651-50	Sequence 50, Appl
34	1201.5	48.7	1916	7	US -10-108-260A-1166	Sequence 1166, Ap
35	1201.5	48.7	3076	9	US -10-723-860-5256	Sequence 5256, Ap
36	1173	47.5	739	10	US -10-450-763-26457	Sequence 26457, A
37	1156	46.8	1913	7	US -10-225-810-40	Sequence 40, Appl
38	1088	44.1	986	7	US -10-225-810-50	Sequence 50, Appl
39	989.5	40.1	1615	8	US -10-415-378-30	Sequence 30, Appl
40	866	35.1	2036	13	US -11-097-143-26834	Sequence 26834, A
41	861	34.9	1863	13	US -11-097-143-31109	Sequence 31109, A
42	861	34.9	2140	13	US -11-097-143-26192	Sequence 26192, A
43	826	33.5	13894	7	US -10-225-810-8	Sequence 8, Appli
44	790	32.0	4291	13	US -11-097-143-31108	Sequence 31108, A
45	790	32.0	5956	13	US -11-097-143-26191	Sequence 26191, A

ALIGNMENTS

```
RESULT 1
US-10-120-988-9
; Sequence 9, Application US/10120988
; Publication No. US20030219745A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT: Goodrich, Ryle
;  APPLICANT: Liu, Chenghua
;  APPLICANT: Ren, Feiyan
;  APPLICANT: Wang, Dunrui
;  APPLICANT: Drmanac, Radoje T.
;  TITLE OF INVENTION: No. US20030219745A1el Nucleic Acids and
```

SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-2.p2n.rnpbn.

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-2.p2n.rnpbn.

start

```
                    GenCore version 5.1.9
          Copyright (c) 1993  - 2006  Bioacceleration Ltd.


OM protein - nucleic search, using frame_plus_p2n model

Run on:         August  7, 2006, 14:51:51 ; Search time 235 Seconds
                                   (without alignments)
                                   4812.163 Million cell updates/sec

Title:          US -10-679-362-2
Perfect score:  2469
Sequence:       1 MSTQRLRNEDYHDYSSTDVS.........YELIQPSNAPIFINSTCAFI 476

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       2193277 seqs, 791917567 residues

Total number of hits satisfying chosen parameters:     4386554

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model  -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10679362/runat_07082006_113054_26104/app_query.fasta_1
-DB=Published_Applications_NA_New  -QFMT=fastap  -SUFFIX=p2n.rnpbn  -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss03h
-USER=US10679362_@CGN_1_1_207_@runat_07082006_113054_26104  -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      Published_Applications_NA_New:*
                1:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                6:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                7:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                8:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
                9:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
                10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2469	100.0	5821	8	US -11-266-748A-31080	Sequence 31080, A
	2	2469	100.0	5821	8	US -11-266-748A-56815	Sequence 56815, A
	3	2469	100.0	5823	8	US -11-266-748A-28306	Sequence 28306, A
	4	1255.5	50.9	2426	6	US -10-505-928-27	Sequence 27, Appl
	5	1255.5	50.9	2493	8	US -11-266-748A-31287	Sequence 31287, A
	6	1244.5	50.4	1869	8	US -11-266-748A-27590	Sequence 27590, A
	7	1201.5	48.7	1916	8	US -11-293-697-1166	Sequence 1166, Ap
	8	552.5	22.4	1625	8	US -11-266-748A-94144	Sequence 94144, A
	9	552.5	22.4	1625	8	US-11-266-748A-113171	Sequence 113171,
c	10	552.5	22.4	1625	8	US -11-266-748A-146955	Sequence 146955,
c	11	503	20.4	586	8	US -11-266-748A-94145	Sequence 94145, A
c	12	503	20.4	586	8	US -11-266-748A-113172	Sequence 113172,
	13	503	20.4	586	8	US -11-266-748A-146956	Sequence 146956,
	14	468	19.0	1588	6	US -10-953-349-367	Sequence 367, App
	15	465.5	18.9	2142	8	US -11-217-529-78323	Sequence 78323, A
	16	453.5	18.4	2154	8	US -11-217-529-2181	Sequence 2181, Ap
	17	418	16.9	2160	8	US -11-217-529-4562	Sequence 4562, Ap
	18	410.5	16.6	494	8	US -11-266-748A-351476	Sequence 351476,
c	19	410.5	16.6	494	8	US -11-266-748A-434855	Sequence 434855,
	20	405	16.4	1500	6	US -10-449-902-8554	Sequence 8554, Ap
	21	405	16.4	1514	6	US -10-449-902-20813	Sequence 20813, A
	22	404.5	16.4	1756	6	US -10-449-902-4377	Sequence 4377, Ap
	23	404.5	16.4	2089	6	US -10-449-902-25208	Sequence 25208, A
	24	402.5	16.3	2977	6	US -10-449-902-25143.	Sequence 25143, A
	25	400	16.2	1405	6	US -10-449-902-786	Sequence 786, App
	26	392.5	15.9	2200	9	US -11-218-305-9533	Sequence 9533, Ap
	27	387.5	15.7	2079	8	US -11-217-529-77476	Sequence 77476, A
	28	386.5	15.7	1697	6	US -10-449-902-4221	Sequence 4221, Ap
	29	379.5	15.4	1984	6	US -10-449-902-14209	Sequence 14209, A
	30	352.5	14.3	1381	6	US -10-449-902-8460	Sequence 8460, Ap
	31	323.5	13.1	1354	8	US -11-145-307A-6	Sequence 6, Appli
	32	320	13.0	2000	9	US -11-174-307B-5169	Sequence 5169, Ap
	33	307.5	12.5	1623	9	US -11-056-355B-54598	Sequence 54598, A
	34	302	12.2	2007	9	US -11-056-355B-105674	Sequence 105674,
	35	302	12.2	2007	9	US -11-056-355B-116913	Sequence 116913,
	36	296	12.0	2160	9	US -11-218-305-13745	Sequence 13745, A
	37	292	11.8	1534	6	US -11-218-305-13746	Sequence 13746, A
	38	292	11.8	1829	9	US -11-056-355B-79661	Sequence 79661, A
	39	291.5	11.8	1614	9	US -11-056-355B-75676	Sequence 75676, A
	40	290	11.7	2112	9	US -11-218-305-10108	Sequence 10108, A
	41	281	11.4	2011	9	US -11-056-355B-96648	Sequence 96648, A
	42	276	11.2	2010	9	US -11-056-355B-36516	Sequence 36516, A
	43	276	11.2	2010	9	US -11-056-355B-44878	Sequence 44878, A
	44	268.5	10.9	1859	6	US -10-953-349-34885	Sequence 34885, A
	45	268.5	10.9	1859	9	US -11-056-355B-8579	Sequence 8579, Ap

ALIGNMENTS

RESULT 1
US-11-266-748A-31080
; Sequence 31080, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815 -0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005 -11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004 -11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004 -11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4

SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-1.rnpbm.

Score Home Page	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-1.rnpbm.

start

Go Back to previous page

```
                         GenCore version 5.1.9
               Copyright (c) 1993  - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:          August  7, 2006, 14:01:19 ; Search time 2620 Seconds
                                             (without alignments)
                                             9816.038 Million cell updates/sec

Title:           US -10-679-362-1
Perfect score:   2093
Sequence:        1 cgggcagcaaaggaggatgg..........aaaaaaaaaaaaaaaaaaaa 2093

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:      37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_NA_Main:*
                 1:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 6:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 7:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 8:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 9:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 10:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                 11:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                 12:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                 13:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                 14:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
                 15:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
                 16:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result          Query
  No.    Score Match Length DB  ID                    Description
----------------------------------------------------------------------
   1    2093  100.0   2093  3   US -09-805-456-1        Sequence 1, Appli
```

```
       2     2093   100.0    2093   8  US -10-679-362-1              Sequence 1, Appli
       3    1847.6   88.3    2055   7  US -10-225-810-5              Sequence 5, Appli
       4    1806.4   86.3    5821  10   US -10-887-553A-1194          Sequence 1194, Ap
       5    1609.8   76.9    3114   8  US -10-332-447-40             Sequence 40, Appl
       6    1541.8   73.7    1961   7  US -10-094-749-1437           Sequence 1437, Ap
       7    1498.4   71.6    1597   7  US -10-120-988-9              Sequence 9, Appli
       8    1441.8   68.9    1501   7  US -10-080-334-21             Sequence 21, Appl
       9    1363.8   65.2    1513   7  US -10-080-334-19             Sequence 19, Appl
      10    1125.8   53.8    1824   7  US -10-225-810-42             Sequence 42, Appl
      11    1113.8   53.2    2034   7  US -10-225-810-2              Sequence 2, Appli
      12     869.2   41.5    2142   8  US -10-467-685-27             Sequence 27, Appl
      13     867.6   41.5    3434   7  US -10-225-810-3              Sequence 3, Appli
      14     866     41.4    1464   7  US -10-392-219-1              Sequence 1, Appli
      15     830.2   39.7    2436   7  US -10-225-810-6              Sequence 6, Appli
      16     830.2   39.7    2436   7  US -10-225-810-55             Sequence 55, Appl
      17     829.8   39.6    2456   7  US -10-225-810-13             Sequence 13, Appl
      18     769.6   36.8     947   9  US -10-357-930-23233          Sequence 23233, A
      19     769.6   36.8     947   9  US -10-357-930-29106          Sequence 29106, A
      20     729.8   34.9    1703   7  US -10-225-810-4              Sequence 4, Appli
      21     727.4   34.8     953   7  US -10-080-334-23             Sequence 23, Appl
      22     721.8   34.5    1473   6  US -10-291-737-1              Sequence 1, Appli
      23     721.8   34.5    1473   7  US -10-365-564-1              Sequence 1, Appli
      24     682     32.6    1752   7  US -10-225-810-1              Sequence 1, Appli
      25     681.8   32.6     739  10   US -10-450-763-26457          Sequence 26457, A
   c  26     645.2   30.8   77992   7  US -10-225-810-11             Sequence 11, Appl
   c  27     645.2   30.8  250000   7  US -10-225-810-26             Sequence 26, Appl
      28     634.2   30.3   46649   3  US -09-805-456-3              Sequence 3, Appli
      29     634.2   30.3   46649   8  US -10-679-362-3              Sequence 3, Appli
      30     586.4   28.0    1913   7  US -10-225-810-40             Sequence 40, Appl
      31     569.8   27.2     986   7  US -10-225-810-50             Sequence 50, Appl
      32     454.8   21.7    1615   8  US -10-415-378-30             Sequence 30, Appl
      33     422     20.2    3351   9  US -10-357-930-20872          Sequence 20872, A
      34     422     20.2    3351   9  US -10-357-930-21002          Sequence 21002, A
      35     422     20.2    3351   9  US -10-357-930-26718          Sequence 26718, A
      36     422     20.2    3351   9  US -10-357-930-26844          Sequence 26844, A
   c  37     390.4   18.7     551  10   US -10-450-763-26458          Sequence 26458, A
      38     379.6   18.1    1455   6  US -10-055-025-3              Sequence 3, Appli
      39     379.6   18.1    1455   7  US -10-154-419-93             Sequence 93, Appl
      40     379.6   18.1    1455  16   US -11-043-889-53             Sequence 53, Appl
      41     379.6   18.1    2397   6  US -10-055-025-1              Sequence 1, Appli
      42     379.6   18.1    2397   7  US -10-154-419-91             Sequence 91, Appl
      43     379.6   18.1    2397  16   US -11-043-889-51             Sequence 51, Appl
      44     379.6   18.1    2423   6  US -10-098-841-260            Sequence 260, App
      45     379.6   18.1    2905   8  US -10-755-889-21             Sequence 21, Appl
```

                                ALIGNMENTS

RESULT 1
US-09-805-456-1
; Sequence 1, Application US/09805456
; Publication No. US20030170778A1
; GENERAL INFORMATION:
;   APPLICANT: WEI, Ming -Hui
;   TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
;   TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: CL001062
;   CURRENT APPLICATION NUMBER: US/09/805,456
;   CURRENT FILING DATE: 2001 -03-14
;   NUMBER OF SEQ ID NOS: 7
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2093
;   TYPE: DNA
;   ORGANISM: Human
US-09-805-456-1

  Query Match   100.0%; Score 2093; DB 3; Length 2093;
  Best Local Similarity   100.0%; Pred. No. 0;
  Matches 2093; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CGGGCAGCAAAGGAGGATGGCGAGGGGCTGATACTGAACCCGGGAAGGGTGGGCTGTGCT 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CGGGCAGCAAAGGAGGATGGCGAGGGGCTGATACTGAACCCGGGAAGGGTGGGCTGTGCT 60

SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-1.rnpbn.

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-1.rnpbn.

start

```
                         GenCore version 5.1.9
             Copyright (c) 1993  - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:          August  7, 2006, 14:01:46 ; Search time 369 Seconds
                                             (without alignments)
                                             8983.650 Million cell updates/sec

Title:           US -10-679-362-1
Perfect score:   2093
Sequence:        1 cgggcagcaaaggaggatgg..........aaaaaaaaaaaaaaaaaaaa 2093

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2193277 seqs, 791917567 residues

Total number of hits satisfying chosen parameters:     4386554

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_NA_New:*
                 1:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 6:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 7:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                 8:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
                 9:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                           SUMMARIES
                     %
Result              Query
   No.    Score   Match Length DB  ID                    Description
-------------------------------------------------------------------------------
     1   1806.4   86.3   5821   8  US -11-266-748A-31080   Sequence 31080, A
     2   1806.4   86.3   5821   8  US -11-266-748A-56815   Sequence 56815, A
     3   1806     86.3   5823   8  US -11-266-748A-28306   Sequence 28306, A
     4    379.6   18.1   2426   6  US -10-505-928-27       Sequence 27, Appl
     5    379.6   18.1   2493   8  US -11-266-748A-31287   Sequence 31287, A
     6    374.8   17.9   1869   8  US -11-266-748A-27590   Sequence 27590, A
     7    338.8   16.2   1916   8  US -11-293-697-1166     Sequence 1166, Ap
```

	8	152	7.3	1625	8	US -11-266-748A-94144	Sequence 94144, A
	9	152	7.3	1625	8	US -11-266-748A-113171	Sequence 113171,
c	10	152	7.3	1625	8	US -11-266-748A-146955	Sequence 146955,
c	11	151.8	7.3	586	8	US -11-266-748A-94145	Sequence 94145, A
c	12	151.8	7.3	586	8	US -11-266-748A-113172	Sequence 113172,
	13	151.8	7.3	586	8	US -11-266-748A-146956	Sequence 146956,
	14	137.8	6.6	494	8	US -11-266-748A-351476	Sequence 351476,
c	15	137.8	6.6	494	8	US -11-266-748A-434855	Sequence 434855,
	16	125.6	6.0	2627	8	US -11-266-748A-26574	Sequence 26574, A
	17	122.8	5.9	2671	8	US -11-266-748A-26827	Sequence 26827, A
	18	121.4	5.8	4086	8	US -11-266-748A-24494	Sequence 24494, A
	19	121	5.8	1000	8	US -11-266-748A-223756	Sequence 223756,
	20	121	5.8	1000	8	US -11-266-748A-291819	Sequence 291819,
c	21	121	5.8	1000	8	US -11-266-748A-343248	Sequence 343248,
	22	121	5.8	1000	8	US -11-266-748A-403361	Sequence 403361,
c	23	121	5.8	1000	8	US -11-266-748A-474407	Sequence 474407,
	24	121	5.8	1885	8	US -11-266-748A-28499	Sequence 28499, A
	25	121	5.8	7644	8	US -11-266-748A-56314	Sequence 56314, A
	26	120.8	5.8	1000	8	US -11-266-748A-398969	Sequence 398969,
c	27	120.8	5.8	1000	8	US -11-266-748A-470015	Sequence 470015,
	28	120.6	5.8	3532	8	US -11-266-748A-28445	Sequence 28445, A
	29	120.4	5.8	4930	8	US -11-266-748A-24488	Sequence 24488, A
	30	120.2	5.7	863	8	US -11-266-748A-224047	Sequence 224047,
	31	120.2	5.7	863	8	US -11-266-748A-404202	Sequence 404202,
c	32	120.2	5.7	863	8	US -11-266-748A-475248	Sequence 475248,
	33	120.2	5.7	1000	8	US -11-266-748A-289413	Sequence 289413,
	34	120.2	5.7	1000	8	US -11-266-748A-294462	Sequence 294462,
c	35	120.2	5.7	1000	8	US -11-266-748A-340842	Sequence 340842,
c	36	120.2	5.7	1000	8	US -11-266-748A-345891	Sequence 345891,
	37	120.2	5.7	1000	8	US -11-266-748A-400446	Sequence 400446,
	38	120.2	5.7	1000	8	US -11-266-748A-406746	Sequence 406746,
c	39	120.2	5.7	1000	8	US -11-266-748A-471492	Sequence 471492,
c	40	120.2	5.7	1000	8	US -11-266-748A-477792	Sequence 477792,
	41	120.2	5.7	1725	8	US -11-266-748A-26586	Sequence 26586, A
	42	120.2	5.7	2578	8	US -11-266-748A-30590	Sequence 30590, A
	43	120.2	5.7	2623	8	US -11-266-748A-57608	Sequence 57608, A
	44	120.2	5.7	2688	8	US -11-266-748A-26340	Sequence 26340, A
	45	120	5.7	1000	8	US -11-266-748A-222640	Sequence 222640,

ALIGNMENTS

RESULT 1
US-11-266-748A-31080
; Sequence 31080, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815 -0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005 -11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004 -11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004 -11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004 -11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004 -11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004 -11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004 -11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005 -03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005 -07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31080
;   LENGTH: 5821